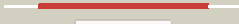



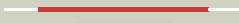

















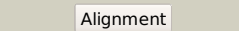









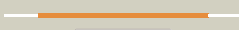


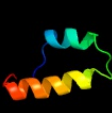





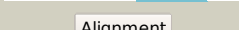

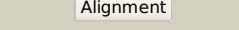
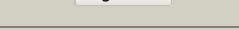
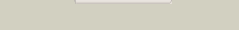
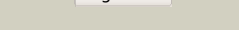
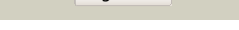


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1246c_(-)_1388691_1388984
Date	Wed Jul 31 22:05:33 BST 2019
Unique Job ID	3cde21ed08cc98fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g5oC_	 Alignment		99.9	54	PDB header: toxin/antitoxin Chain: C; PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
2	c3bpqD_	 Alignment		99.9	17	PDB header: toxin Chain: D; PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
3	c2kheA_	 Alignment		99.9	28	PDB header: hydrolase Chain: A; PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
4	c3kixy_	 Alignment		99.9	20	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)
5	d1wmia1	 Alignment		99.9	29	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
6	c2otrA_	 Alignment		99.6	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein hp0892; PDBTitle: solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
7	c3oeiH_	 Alignment		99.4	25	PDB header: toxin, protein binding Chain: H; PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
8	d2a6sa1	 Alignment		99.3	21	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
9	d1z8ma1	 Alignment		99.1	15	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
10	c4q2uH_	 Alignment		98.9	15	PDB header: toxin/toxin repressor Chain: H; PDB Molecule: mrna interferase yafq; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
11	c5cegB_	 Alignment		98.3	17	PDB header: toxin Chain: B; PDB Molecule: plasmid stabilization system; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum

12	c5cw7H_	 Alignment		98.0	20	PDB header: toxin Chain: H: PDB Molecule: plasmid stabilization protein pare; PDBTitle: crystal structure of the paaa2-pare2 antitoxin-toxin complex
13	c3kxeB_	 Alignment		97.8	27	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
14	c4mctD_	 Alignment		97.4	18	PDB header: toxin Chain: D: PDB Molecule: killer protein; PDBTitle: p. vulgaris higba structure, crystal form 1
15	c5ja9D_	 Alignment		96.9	17	PDB header: toxin Chain: D: PDB Molecule: toxin higb-2; PDBTitle: crystal structure of the higb2 toxin in complex with nb6
16	c6f8sD_	 Alignment		94.1	14	PDB header: toxin Chain: D: PDB Molecule: putative killer protein; PDBTitle: toxin-antitoxin complex grata
17	c5ifgC_	 Alignment		80.2	15	PDB header: hydrolase/antitoxin Chain: C: PDB Molecule: mrna interferase higb; PDBTitle: crystal structure of higb-higb complex from e. coli
18	c2kruA_	 Alignment		60.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: solution nmr structure of the pcp_red domain of light-independent2 protochlorophyllide reductase subunit b from chlorobium tepidum.3 northeast structural genomics consortium target ctr69a
19	c2l09A_	 Alignment		50.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: asr4154 protein; PDBTitle: solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
20	c6avhA_	 Alignment		38.5	19	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
21	c4b2gB_	 Alignment	not modelled	38.2	19	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
22	c4ewvB_	 Alignment	not modelled	36.3	19	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
23	c4ep1A_	 Alignment	not modelled	33.3	19	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
24	c2lc0A_	 Alignment	not modelled	28.1	10	PDB header: protein binding Chain: A: PDB Molecule: putative uncharacterized protein tb39.8; PDBTitle: rv0020c_nter structure
25	d1ugja_	 Alignment	not modelled	27.5	18	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: RIKEN cDNA 2310057j16 protein (KIAA1543)
26	c5kodA_	 Alignment	not modelled	26.5	21	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
27	d2pu9b1	 Alignment	not modelled	20.7	20	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
28	c5m5cC_	 Alignment	not modelled	19.8	18	PDB header: transport protein Chain: C: PDB Molecule: calmodulin-regulated spectrin-associated protein 1; PDBTitle: mechanism of microtubule minus-end recognition and

						protection by2 camsap proteins
29	c2apnA_	Alignment	not modelled	10.2	27	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
30	d1nwba_	Alignment	not modelled	9.0	9	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
31	c4xukB_	Alignment	not modelled	8.8	22	PDB header: hydrolase Chain: B; PDB Molecule: putative hydrolase; PDBTitle: crystal structure of hydrolase aboph in beta lactamase superfamily
32	c2ynmD_	Alignment	not modelled	8.6	9	PDB header: oxidoreductase Chain: D; PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
33	c4le6B_	Alignment	not modelled	8.5	21	PDB header: hydrolase Chain: B; PDB Molecule: organophosphorus hydrolase; PDBTitle: crystal structure of the phosphotriesterase ophc2 from pseudomonas2 pseudoalcaligenes
34	d1xqba_	Alignment	not modelled	6.5	17	Fold: YaeB-like Superfamily: YaeB-like Family: YaeB-like
35	d3bzka5	Alignment	not modelled	6.5	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
36	d1s98a_	Alignment	not modelled	6.2	13	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
37	c2d2aA_	Alignment	not modelled	5.9	29	PDB header: metal transport Chain: A; PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in biosynthesis of2 iron-sulfur clusters
38	c2h5gA_	Alignment	not modelled	5.8	17	PDB header: oxidoreductase Chain: A; PDB Molecule: delta 1-pyrroline-5-carboxylate synthetase; PDBTitle: crystal structure of human pyrroline-5-carboxylate synthetase
39	c1hk7A_	Alignment	not modelled	5.8	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp82; PDBTitle: middle domain of hsp90
40	c1x0gA_	Alignment	not modelled	5.7	43	PDB header: metal binding protein Chain: A; PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
41	c2k4zA_	Alignment	not modelled	5.3	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr::2 northeast structural genomics consortium target op5